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OCT 03 2003  
FEDERAL TRADE COMMISSION

1600

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/759,990A  
DATE: 09/30/2003  
TIME: 10:27:48

Input Set : E:\31276-20026.00 - seqlist (final) fixed.txt  
Output Set: N:\CRF4\09302003\I759990A.raw

3 <110> APPLICANT: AntiCancer, Inc.  
4 Xu, Mingxu  
5 Han, Oinghong  
7 <120> TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGH  
8 SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLHOMOCYSTAINASE  
9 (SAHH) AND IMPROVED ASSAYS FOR S-ADENOSYLMETHIONINE (SAM)  
12 <130> FILE REFERENCE: 31276-20026.00  
14 <140> CURRENT APPLICATION NUMBER: US 09/759,990A  
15 <141> CURRENT FILING DATE: 2001-01-12  
17 <150> PRIOR APPLICATION NUMBER: US 60/176,444  
18 <151> PRIOR FILING DATE: 2000-01-14  
20 <160> NUMBER OF SEQ ID NOS: 7  
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 1461  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Homo sapiens (nucleotide sequence of SAHH)  
29 <400> SEQUENCE: 1  
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31 catgttctcg gccgttaagga acttaccctt gctgagaagg aaatgcagg tcttatgggt 120  
32 cttcgtgagc gttattccgc ttctaaagcca ttgaagggtg tcagaatctc tgggtccctc 180  
33 cacatgacag tccagacagc cgtcctcatc gagacactca cagctcttgg tgctgtatgc 240  
34 agatgggctt cctgcaacat cttctctaca caagatacag ccgctgtgc tattgttgc 300  
35 gggccaaacag gcacacccaga gaagccagcc ggtatcccaq tcttcgctg gaagggcgaa 360  
36 acactcccag aatactggga gaacacatac cgcgtctca catggccaga tggtcaaggc 420  
37 ccacagcagg ttgtcgatga tgggtgtat gctacactcc tcatctccaa gggcttcgaa 480  
38 ttgcggaaacag ccgggtctgt tccagagcca acagaagctg acaacccatc ataccgtgc 540  
39 gttcttgcta cactcaagca ggttcaac caagacaaga accactggca cacagttgt 600  
40 gccggcatga acgggttttc cgaagagaca acaacagggt tccaccgcctt ctaccagtc 660  
41 gagaaggagg gcaaaactctt cttcccgcc atcaacgtca acgacgtgt tacaaggatcc 720  
42 aagttcgata acatctacgg ctgcggccac tcccttatcg atggatcaa ccgtgttcc 780  
43 gatgtcatga tcggcgccaa gacagctctc gtcatgggtt acggcgatgt cggcaaggcc 840  
44 tgcgctcaat ccctccgtgg ccaaggcgct cgcgttatca tcacagaact cgacccaaatc 900  
45 tgcgctctcc aggctgcccatt ggaaggctac caggtccgc gcatcgagga agtgcgtcaag 960  
46 gatgtcgata tcttcgttac atgcacagga aactgcgata tcatctctgt tgacatgtat 1020  
47 gcccagatga aggataaggc tattgtcggt aacatcgcc acgtcgataa cggaaattgtat 1080  
48 acagatggcc tcataaata cccaggcatc aagcacatcc caatcaagcc agaatacgac 1140  
49 atgtggaaat tcccgatgg ccacgtatc ctccttcttg ctgaggcccg ccttcttaac 1200  
50 cttggctgctc ctacaggatca cccatcttcc gttatgtcaa tgtcattcac aaaccagaca 1260  
51 ctcgctcagc tcgacctcta cggaaagaga gaaatctcg agaagaaggt ttacacactt 1320  
52 cccaaaggatc tcgatgaaga agtcgctcgc ctccacctcg gatctctcga tgtccaccc 1380  
53 acaaaggatca cacagaagca ggctgactac atcaacgttc cagttgaggg tccttacaag 1440  
54 tctgtatgtt accgttattaa a 1461

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58 <210> SEQ ID NO: 2
59 <211> LENGTH: 33
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Upstream primer
66 <400> SEQUENCE: 2
67 ttttggatcc gcttgcaaat cacctgctgg tgc 33
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71 <211> LENGTH: 24
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Downstream primer
78 <400> SEQUENCE: 3
79 ttttctgcag ggggagctat cgct 24
81 <210> SEQ ID NO: 4
82 <211> LENGTH: 38
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: Primer
89 <400> SEQUENCE: 4
90 catcatcatc atcatcacgc ttgcaaatca cctactgg 38
93 <210> SEQ ID NO: 5
94 <211> LENGTH: 30
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Primer
101 <400> SEQUENCE: 5
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105 <210> SEQ ID NO: 6
106 <211> LENGTH: 1461
107 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens (nucleotide sequence of SAHH - wild type)
110 <400> SEQUENCE: 6
111 atggcttgc aatcacctgc tgggtctcca ttgcgttaca gaattgccga catcaaccc 60
112 catgttctcg gccgtaagga acttaccctt gctgagaagg aatgccagg tcttatggtt 120
113 cttcgtgagc gttattccgc ttctaagcca ttgaagggtg tcagaatctc tggttccctc 180
114 cacatgacag tccagacagc ggtccttatt gagacactca cagcttgg tgctgatgtc 240
115 agatgggctt cctgcaacat ctctctaca caagatacg ccgctgtgc tattcgttgc 300
116 ggcccaacag gcacaccaga gaagccagcc ggtatcccg tcttcgttgc gaaaggcgaa 360
117 acactcccaag aatactggga gaacacatac cgcgtctca catggccaga tggtaaggc 420
118 ccacagcagg ttgtcgatga tgggtgtat gctacactcc tcatttccaa gggcttcgaa 480
119 ttgcgaaacag ccgggtgtgt cccagagcca acagaagctg acaacctcga ataccgctgc 540
120 gttcttgcta cactcaagca ggttcaac caagacaaga accactggca cacagttgtc 600
121 gccggcatga acggtgtttc cgaagagaca acaacagggtg tccaccgcct ctaccagctc 660
122 gagaaggagg gcaaactcct cttcccgagcc atcaacgtca acgacgctgt tacaaagtcc 720
  
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123	aagttcgata	acatctacgg	ctgtcgccac	tcccttac	atggtatcaa	ccgtgcttcc	780										
124	gatgtcatga	tcggcggcaa	gacagctctc	gtcatgggt	acggcgatgt	cgggaagggc	840										
125	tgcgctcaat	ccctccgtgg	ccaaggcgct	cgcgttatca	tcacagaact	cgaccctatc	900										
126	tgcgctctcc	aggctgtcat	ggaaggctac	caggtccgcc	gcatcgagga	agtctgtcaag	960										
127	gatgtcgata	tcttcgttac	atgcacagga	aactgcgata	tcatctctgt	tgacatgtat	1020										
128	gcccgatgt	aggataaggc	tattgtcggt	aacatcgcc	acttcgataa	cgaatttgat	1080										
129	acagatggcc	tcatgaaata	cccaggcatc	aagcacatcc	caatcaagcc	agaatacgac	1140										
130	atgtggaaat	tcccagatgg	ccacgctatc	ctcccttctt	ctgagggccg	ccttcttaac	1200										
131	cttgggttgcg	ctacaggctca	cccatcttcc	gttatgtcaa	tgtcattcac	aaaccagaca	1260										
132	ctcgctcagc	tcgacccctca	cgaaaagaga	ggaaatctcg	agatgaaggt	ttacacactt	1320										
133	ccgaagcattc	tcgatgaaga	agtcgttcgc	ctccacctcg	gatctctcg	tgtccacctt	1380										
134	acaaagctta	cacagaagca	ggctgactac	atcaacgttc	cagttgaggg	tccttacaag	1440										
135	tctgatgctt	accgttatta	a				1461										
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141	<213>	ORGANISM:	Homo sapiens														
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145	1						5			10					15		
146	Asp	Ile	Asn	Leu	His	Val	Leu	Gly	Arg	Lys	Glu	Leu	Thr	Leu	Ala	Glu	
147							20			25				30			
148	Lys	Glu	Met	Pro	Gly	Leu	Met	Val	Leu	Arg	Glu	Arg	Tyr	Ser	Ala	Ser	
149							35			40				45			
150	Lys	Pro	Leu	Lys	Gly	Val	Arg	Ile	Ser	Gly	Ser	Leu	His	Met	Thr	Val	
151							50			55				60			
152	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala	Leu	Gly	Ala	Asp	Val	
153	65						70			75				80			
154	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln	Asp	Thr	Ala	Ala	Ala	
155							85			90				95			
156	Ala	Ile	Val	Val	Gly	Pro	Thr	Gly	Thr	Pro	Glu	Lys	Pro	Ala	Gly	Ile	
157							100			105				110			
158	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Thr	Leu	Pro	Glu	Tyr	Trp	Glu	Asn	
159							115			120				125			
160	Thr	Tyr	Arg	Ala	Leu	Thr	Trp	Pro	Asp	Gly	Gln	Gly	Pro	Gln	Gln	Val	
161							130			135				140			
162	Val	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Leu	Leu	Ile	Ser	Lys	Gly	Phe	Glu	
163	145						145			150				155			160
164	Phe	Glu	Thr	Ala	Gly	Ala	Val	Pro	Glu	Pro	Thr	Glu	Ala	Asp	Asn	Leu	
165							165			170				175			
166	Glu	Tyr	Arg	Cys	Val	Leu	Ala	Thr	Leu	Lys	Gln	Val	Phe	Asn	Gln	Asp	
167							180			185				190			
168	Lys	Asn	His	Trp	His	Thr	Val	Ala	Ala	Gly	Met	Asn	Gly	Val	Ser	Glu	
169							195			200				205			
170	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	Gln	Leu	Glu	Lys	Glu	Gly	
171							210			215				220			
172	Lys	Leu	Leu	Phe	Pro	Ala	Ile	Asn	Val	Asn	Asp	Ala	Val	Thr	Lys	Ser	
173	225						225			230				235			240
174	Lys	Phe	Asp	Asn	Ile	Tyr	Gly	Cys	Arg	His	Ser	Leu	Ile	Asp	Gly	Ile	

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175	245	250	255
176	Asn Arg Ala Ser Asp Val Met Ile Gly Gly Lys Thr Ala Leu Val Met		
177	260	265	270
178	Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Gln Ser Leu Arg Gly Gln		
179	275	280	285
180	Gly Ala Arg Val Ile Ile Thr Glu Leu Asp Pro Ile Cys Ala Leu Gln		
181	290	295	300
182	Ala Ala Met Glu Gly Tyr Gln Val Arg Arg Ile Glu Glu Val Val Lys		
183	305	310	315
184	320	325	330
185	Asp Val Asp Ile Phe Val Thr Cys Thr Gly Asn Cys Asp Ile Ile Ser		
186	335	340	345
187	Val Asp Met Met Ala Gln Met Lys Asp Lys Ala Ile Val Gly Asn Ile		
188	350	355	360
189	365	370	375
190	Gly Ile Lys His Ile Pro Ile Lys Pro Glu Tyr Asp Met Trp Glu Phe		
191	380	385	390
192	395	400	405
193	410	415	420
194	425	430	435
195	440	445	450
196	455	460	465
197	470	475	480
198	485		
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200			
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203			
204			
205			

**VERIFICATION SUMMARY**

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Input Set : E:\31276-20026.00 - seqlist (final) fixed.txt  
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